CHARACTERIZATION OF *N* GENE HOMOLOGS IN *NICOTIANA* SPECIES, <u>Kim.A. Palmer</u>, B.E. Wiggins, C.A. Angel, B. Balaji, and J.E. Schoelz*, University of Missouri - Columbia, Department of Plant Pathology and Microbiology, Columbia, MO 65205, Bier, Karla <u>kbier@stephens.edu</u>

Tomato bushy stunt virus (TBSV) is an important plant pathogen in Missouri. We are working to understand genes involved in TBSV resistance and develop methods for transferring TBSV resistance genes between plants. A new variety of *Nicotiana*, *N. edwardsonii* var. Columbia will be described. It can be used as a bridge plant to move virus resistance genes from *N. glutinosa* to *N. clevelandii*. To characterize a single dominant gene that specifies resistance to TBSV, we have made crosses between *N. edwardsonii*. var. Columbia and *N. clevelandii*. A gene silencing assay has been developed which targets host resistance genes in the NBS-LRR category and have used this assay to show that the TBSV resistance gene has sequence similarity to the *N* resistance gene. To examine the diversity of *N* gene homolog sequences that exist, we developed PCR primers that amplified a 516 bp DNA segment of Exon 2 of the *N* gene. This PCR reaction yielded multiple products, which were cloned and sequenced. In *N. clevelandii*, two *N* homologs predominated. These sequences differed from the *N* gene by approximately 10%. The analysis of n homologs in *N. glutinosa* is still being completed, but preliminary results indicate that this *Nicotiana* species contains a broader array of *N* gene homologs than *N. clevelandii*.